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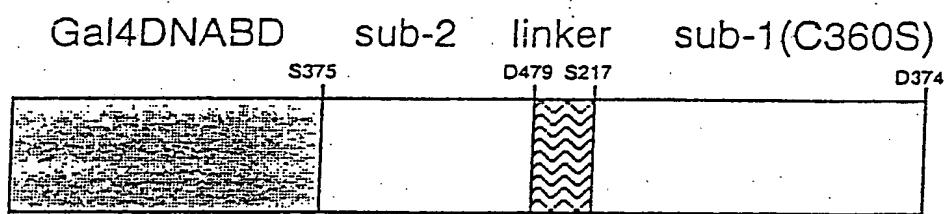


Fig. 1

1/1

CGG CAC GAG GGC CTG GGC AAC GGC CGG CAC ACG CTG GGA CAG CAG GAA GTG GAA GTG GAC  
 R H E G L G N G R H T L G Q Q E V E V D

61/21

GGT CTG ACG GCC TAC GTG GCA GGT GAG CGC CCT GAC CCA CTG GGT CCC AGG TCC CAG CCC  
 G L T A Y V A G E R P D P L G P R S Q P

121/41

GCA TGC CAG GTG GCC CAC GAC CCC CCC AGA AGA GCC TGC CCT CTC TGC TCT CAA GGC ACC AAG  
 A C Q V A H D P P R A C P L C S Q G T K

181/61

ACG CTG AGT GGC AGC ATA GCC CCA ATG AAC GTC TGT GTC CGG GCA CTT Cct GCA GGC CAC  
 T L S G S I A P M N V C V R A L P A G H

241/81

AGG TTC AGC ATG AAG TCG GCC TTG AAG GCT GCA TCC TtG CAC CCC GCC CAG TtG Ctt GCG  
 R F S M K S A L K A S L H P A Q L L G

361/101

CTG GAG AAG AGT AAG GGG ACC TtG ACT TtG GtG CTG ACG CAG ACT TCG TGG TGC TCG ACG  
 L E K S K G T L T L V L T Q T S W C S T

361/121

ACT CCC TtC ACG TCC AGG CCA CCT ACA TCT CGG GTG AGC TGG TGT GGC AGG CGG ACG CAG  
 T P F T S R P T S R V S W C G R T Q

421/141

CTA GGC AGT GAC AAG GAC CTC GGC TGA  
 L S D K D L G \*

31/11

CGG CAC GAG GGC CTG GGC AAC GGC CGG CAC ACG CTG GGA CAG CAG GAA GTG GAA GTG GAC  
 R H E G L G N G R H T L G Q Q E V E V D

91/31

GGT CTG ACG GCC TAC GTG GCA GGT GAG CGC CCT GAC CCA CTG GGT CCC AGG TCC CAG CCC  
 G L T A Y V A G E R P D P L G P R S Q P

151/51

GCA TGC CAG GTG GCC CAC GAC CCC CCC AGA AGA GCC TGC CCT CTC TGC TCT CAA GGC ACC AAG  
 A C Q V A H D P P R A C P L C S Q G T K

211/71

ACG CTG AGT GGC AGC ATA GCC CCA ATG AAC GTC TGT GTC CGG GCA CTT Cct GCA GGC CAC  
 T L S G S I A P M N V C V R A L P A G H

271/91

AGG TTC AGC ATG AAG TCG GCC TTG AAG GCT GCA TCC TtG CAC CCC GCC CAG TtG Ctt GCG  
 R F S M K S A L K A S L H P A Q L L G

331/111

CTG GAG AAG AGT AAG GGG ACC TtG ACT TtG GtG CTG ACG CAG ACT TCG TGG TGC TCG ACG  
 L E K S K G T L T L V L T Q T S W C S T

391/131

ACT CCC TtC ACG TCC AGG CCA CCT ACA TCT CGG GTG AGC TGG TGT GGC AGG CGG ACG CAG  
 T P F T S R P T S R V S W C G R T Q

Fig. 2

1/1

31/11

ggc gcg gct ccg ctc tcg gct ggg gtt cgt cac tgg gcg cgg gat ttg gcc gcc gcg ggg  
 G A A P L S A G V R H W A R D L A A A G  
 61/21 91/31

ctc cgg agc cgc tcg ctc ccg aca ccg ctc acg atg cgc ggc gac agg gcc ggc ggg ggc  
 L R S R S L P T R L T M R G D R A G G G  
 121/41 151/51

ccc gtg ctc cag ttc act aac tgc ccg atc ctg cgc gga ggg aaa ctg ctc agg gag gat  
 P V L Q F T N C R I L R G G K L L R E D  
 181/61 211/71

ctg tgg gtg cgc gga ggc cgc atc ttg gac cca gag aag ctg ttc ttt gag gag cgg cgc  
 L W V R G G R I L D P E K L F F E E R R  
 241/81 271/91

gtg gcc gac gag cgg cgg gac tgc ggg ggc cgc atc ttg gct ccc gga ttc atc gac gtg  
 V A D E R R D C G G R I L A P G F I D V  
 301/101 331/111

cag atc aac cgt gga TTT GGT GTT GAC TTC TCT CAA GCC ACG GAG GAC GTG GGT TCG GGG  
 Q I N R G F G V D F S Q A T E D V G S G  
 361/121 391/131

GTT GCC CTC GTG GCC CGG AGG ATC CTG TCG CAC GGC GTC ACC TCC TTC TGC CCC ACC CTG  
 V A L V A R R I L S H G V T S F C P T L  
 421/141 451/151

GTC ACT TCC CCA CCG GAG GCT TAT CAC AAG GTT GTT CCT CAG ATC CCT GTG AAG AGT GGT  
 V T S P P E A Y H K V V P Q I P V K S G  
 481/161 511/171

GGT CCC CAT GGG GCA GGG GTC CTC GGG CTG CAC CTG GAG GGC CCC TTC ATC AGC CGG GAG  
 G P H G A G V L G L H L E G P F I S R E  
 541/181 571/191

AAG CGG GGC GCG CAC CCC GAG GCC CAC CTC CGC TCC TTC GAG GCC GAT GCC TTC CAG GAC  
 K R G A H P E A H L R S F E A D A F Q D  
 601/201 631/211

TTG CTG GCC ACC TAC GGG CCC CTG GAC AAT GTC CGC ATC GTG ACG CTG GCC CCA GAG TTG  
 L L A T Y G P L D N V R I V T L A P E L  
 661/221 691/231

GGC CGT AGC CAC GAA GTG ATC CGG GCG CTG ACG GCC CGT GGC ATC TGC GTG TCC CTA GGG  
 G R S H E V I R A L T A R G I C V S L G  
 721/241 751/251

CAC TCA GTG GCT GAC CTG CGG GCG GCA GAG GAT GCT GTG TGG AGC GGA GCC ACC TTC ATC  
 H S V A D L R A A E D A V W S G A T F I  
 781/261 811/271

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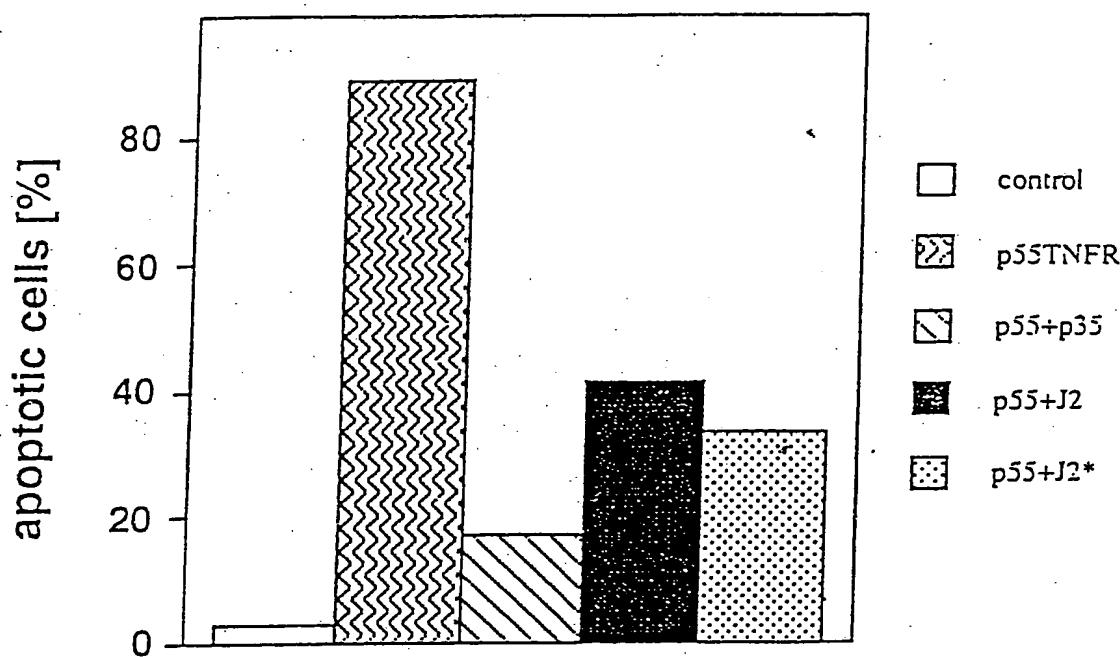
4/19

841/281 871/291  
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901/301 931/311  
ACG CAC ACC AAC CCC GCC GCC CTG CGG ATC GCC CAC CGT GCC CAT CCC CAG GGG CTG GTG  
T H T N P A A L R I A H R A H P Q G L V  
961/321 991/331  
CTG GTC ACC GAT GCC ATC CCT GCC TTG GGC CTG GGC AAC GGC CGG CAC ACG CTG GGA CAG  
L V T D A. I P A L G L G N G R H T L G Q  
1021/341 1051/351  
CAG GAA GTG GAA GTG GAC GGT CTG ACG GCC TAC GTG GCA GGT GAG CGC CCT GAC CCA CTG  
Q E V E V D G L T A Y V A G E R P D P L  
1081/361 1111/371  
GGT CCC AGG TCC CAG CCC GCA TGC CAG GTG GCC CAC GAC CCC CCC AGA GCC TGC CCT CTC  
G P R S Q P A C Q V A H D P P R A C P L  
1141/381 1171/391  
TGC TCT CAA GGC ACC AAG ACG CTG AGT GGC AGC ATA GCC CCA ATG AAC GTC TGT GTC CGG  
C S Q G T K T L S G S I A P M N V C V R  
1201/401 1231/411  
CAC TTC CTG CAG GCC ACA GGC TGC AGC ATG GAG TCG GCC CTG GAG GCT GCA TCC CTG CAC  
H F L Q A T G C S M E S A L E A A S L H  
1261/421 1291/431  
CCC GCC CAG TTG CTG GGG CTG GAG AAG AGT AAG GGG ACC CTG GAC TTT GGT GCT GAC GCA  
P A Q L L G L E K S K G T L D F G A D A  
1321/441 1351/451  
GAC TTC GTG GTG CTC GAC GAC TCC CTT CAC GTC CAG GCC ACC TAC ATC TCG GGT GAG CTG  
D F V V L D D S L H V Q A T Y I S G E L  
1381/461 1411  
GTG TGG CAG GCG GAC GCA GCT AGG CAG TGA CAA GGA CCT CGG CTG AGA GGA CAC CTG GCC  
V W Q A D A A R Q  
1441 1471  
GCA GCG GGA TGC CAT CAG GGC CGG GTG GTT GGG GAG CTG GTC TCC AGG GAG TGA GTC GGG  
1501  
AGC CCT GCT GGA T

Fig. 3 (a)

**A**

## HEK 293-T cells

**B**

## HeLa cells

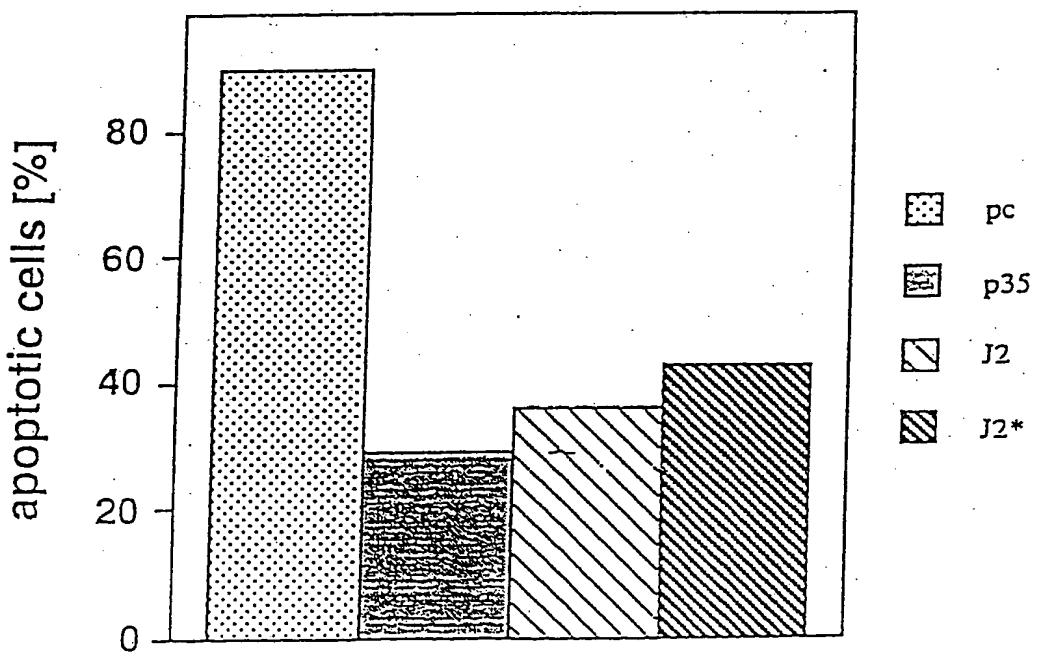


Fig. 4

	1	10	1	20	1	30	1	40	1	50	1	60	1	70	1	80	1	90	1	100
1	GAGCAGCTCA	AAACTCACGT	CCAGGGTGATC	AAGAGGTCAG	CCAAGCCGAG	TGAGGAAGCCC	CGGCTGGGC	AGATAACCCCTC	GGCTGAAGAC	CTGGAGACAG	100									
101	ATGGCGGGG	ACCGGGCCAG	GTGGTGGACG	ATGGCTTGGA	GCACAGGGAG	CTGGGCCATG	GGCAGGCCATG	GGCAGAGGC	CCCGCTCCCTC	TCCAGCAGCA	200									
201	CCCTCAGGTG	TTGCTCTGGG	AACAGCAGCG	ACTGGCTGGG	CGGCTCCCCC	GGGGCAGCAC	CGGGGACACT	GTGGTGGCTTC	CTCTGGCCCA	GGGGGGCAC	300									
301	CGGCCTCTGT	CCCGGGCTCA	GTCTTCCCCA	GCCGACCTG	CCTCACTGTC	AGCCCCAGAG	CCTGGCCAGCC	AGGGCCGAGT	CCTCTCCAGC	TCAGAGACCC	400									
401	CTGCCAGAC	CCTGCCCTTC	ACACACGGGC	TGATCTATGA	CTCGGTCTATG	CTGAAGCACC	AGTGGTCTCTG	CGGTGACAAC	AGCAGGCAAC	CGGAGCACGC	500									
501	CGCCGGCATC	CAGAGCATCT	GGTCCCGGGT	GCAGGGCGG	GGGCTCCGGG	GCCAGTGTGA	GTGTCTCGA	GGCCGGAGG	CCTCCCTTGA	AGAGCTGCAG	600									
601	TCGGTCCACT	CTGAGGGCCA	CGTGGCTCTC	TACGGCACCA	ACCCGGCTAG	CCGGCTCAA	CTGGACAACG	GGAAAGCTGGC	AGGGCTCTTG	GCACAGCGGA	700									
701	TGTTTGTGAT	GCTGCCCTGT	GGTGGGGTTG	GGGTGGACAC	TGACACCATC	TGGAAATGAGC	TTCAATTCTCTC	CAATGCA GCC	CGCTGGGCC	CTGGCAGTGT	800									
801	CACTGACCTC	GCCTTCAGG	TGGCTTCTCG	TGAGGCTAAAG	AATGGTTTTCG	CTGTGGTGGC	GGCCCCAGGA	CACCATGGAG	ATCATTCAC	AGCCATGGGC	900									
901	TTCTGCTTCT	TCAACTCAGT	GGCCATCGCC	TGCCGGCAGC	TGCAACAGCA	GAGCAAGGCC	AGCAAGATCC	TCATTGTAGA	CTGGGACGTG	CACCATGGCA	1000									
1001	ACGGCACCA	GCACAACCTTC	TACCAAGACC	CCAGTGTGCT	CTACATCTCC	CTGCATCGCC	ATGACGCCGG	CAACCTCTTC	CCAGGGAGTG	GGGCTGTGGA	1100									
1101	TGAGGTAAG	GCTGGCAGCG	GTGAGGGCTT	CAATGTCAAT	GTGGCTGGG	CTGGAGGTCT	GGACCCCCC	ATGGGGGATC	CTGAGTACCT	GGCTGCTTTTC	1200									
1201	AGGATAGTCG	TGATGCCAT	CGCCCGAGAG	TTCTCTCCAG	ACCTAGTCCT	GGTGTCTGCT	GGATTGTATG	CTGCTGAGGG	TCACCCGGCC	CCACTGGGTG	1300									
1301	GCTACCATGT	TTCTGCCAAA	TGTTTTGGAT	ACATGACGCA	GCAACTGTATG	AACTCTGGCAG	GAGGGCAGT	GGTGTGGCC	TTGGAGGGTG	GCCATGACCT	1400									
1401	CACAGCCATC	TGTGACGCC	CTGAGGGCTG	TGTGGCTGCT	CTTCTGGTA	ACAGGGTGGA	TCCCCTTTC	GAAGAAGGCT	GGAAACAGAA	ACCCACCCCTC	1500									
1501	AATTCCATCC	GCTCTCTGGA	GGCCGTGATC	CGGGTGCACA	GTAAATAACTG	GGGCTGCATG	CAGGGCCTGG	CCTCCCTGTCC	AGACTCCCTGG	GTGCCCTAGAG	1600									
1601	TGCCAGGGCC	TGACAAANGAA	GAAGTGGAGG	CAGTAACCGC	ACTGGCGTCC	CTCTCTGTGG	GCATCCTGGC	TGAAGATAGG	CCCTGGAGC	AGCTGGTGGA	1700									
1701	GGAGGAAGAA	CCTATGAATC	TCTAA								1725									

Fig. 5A

1	10	1	20	1	30	1	40	1	50	1	60	1	70	1	80	1	90	1	100
1	EQLKTHVQVI	KRSAKPSEKP	RHQIIPSAED	LETGGGPGQ	VVDDGLEHRE	LGHGQPEARQ	PAPLQQHFPQV	LLWEQORLAG	RILPRGSTGDT	VLLPLAQSGH	100								
101	RPLSRAQSSP	AAPASLSAPE	PASQARVLSS	SETPARTLPF	TTGLIYDSVM	LKHQCSCGDN	SRHPEHAGRI	OSIWISRLQER	GLRSQCECLR	GRKASASLEELQ	200								
201	SVHSERHVILL	YGTNPPLSRLK	LDNGKLAGLL	AQRMFVMLPC	GIVGVDTDTI	WNELHSSNAA	RWAAGSVTDL	AFKVASRELK	NGFAVVVRPG	HHADHSTAMG	300								
301	FCFFENSAVIA	CRQLQQSKA	SKILIVDWDV	HHGNNGTQQT	YQDPSVLYIS	LHRHDDGNFF	PGSGAVDEVG	AGSGEGFNVN	VAWAGGLDPP	MGDPPEYLAAF	400								
401	RIVVMPJARE	FSPDVLVSA	GFDAAEGHPA	PLGGYHVS	AKCFCGYMTQQLM	NLAGGAVVLA	LEGGHDLTAI	CDASEACVAA	LLGNRVDPLS	EEGWKQKPNL	500								
501	NSIRSLEAVI	RVHSKYWGCM	QRLASC	CPDSW	VPRVPGADKE	EVEAVTALAS	LSVGILAEDR	PSEQLVEEE	PMNL		574								
1	10	1	20	1	30	1	40	1	50	1	60	1	70	1	80	1	90	1	100

Fig. 5B

	10	20	30	40	50	60	70	80	90	100	
1	M F A R S A G L C F	P W V P G U S H G G	D A E E V L A Q H P	T P T G R G A E R R	P R P P D S S A E G	D P G M L K P C G C	V P S P Q K V A L K	V G A P F C T C G C	F Q R F H I P K A C	P G Q Q G S P E S A	100
101	R P R N R Q P Y A T	Q N G P A P R P Q V	L P G S S S R C H	G Y I C F L F D S S	Q T A E V E V G W G	G D T G S Q L R P I	L R G A V I N S R M	W D S Q K E D S K P	D I L R I Q N T Q L	F H S V S L S T D G	200
201	T Q V S P G A H Y C	S P T G A G G C P R P	C A D T P G P Q P Q	P M D L R V G Q R P	P V E P P P E P T L	L A L Q R P Q R L H	H H L F L A G L Q Q	Q R S V E P M R V K	M E L P A C G A T L	S L V P S L P A F S	300
301	I P R U H Q S Q S S T	P C P F L G C R P C	P Q L S M D T P M P	E L Q V G P Q E Q E	L R Q L L H K D K S	K R S K E V A T P A	Q P S P T S Q V P A	A A C V A C A V A S	S V V K Q Q K L A E V	I L K K Q Q A A L E	400
401	R T V H P N S E G I	P Y R S Q G P C S G	Q C P C S V P T P L	K Q P M H S F C R T	L E P L E T G A T	R S M L S S F L P P	V P S L S P D P P E	H F P L R K T V S E	P N L K L R Y K P K	K S L E R R K N P L	500
501	I R K E S A P P S L	R R R E A T L G D	S S P S S S S T P A	S G C S S P N D S E	H G P N P I L G S E	A L I G Q R L R I Q	E T S V A F A L P	T V S L L P A I T L	G L P A P A R A D S	D R T H P T L G P	600
601	R G P I L G S P H T	P L F L P H G L E P	E A G G T L P S R L	Q P I L L L D P S G	S H A P L L T V P G	L G P L P F H F A Q	S I L M T T E R L S G	S G L H W M P L S R T	R S E P L P P S A T	A P P P P G P M Q P	700
701	R L E Q L K T H V Q	V I K R S A K P S E	K P R L R Q I P S A	E D L I E T D G G P	G Q V V D D G L E H	R E L G H Q P E A	R G P A P L Q Q H P	Q V I L L W E Q Q R L	A G R L P R G S T G	D T V I L L P L A C G	800
801	G H R P L S R A Q S	S P A A P A S L S A	P E P A S Q A R V L	S S S E T P A R T L	P F T T G L I X D S	V M L K H Q C S C G	D N S R R H P E H A G	R I Q S I W S R L Q	E R G L R S Q C E C	L R G R K A S L E E	900
901	L Q S V H S E E H V	L L Y G T N P L S R	I K L D N G K L A G	L L A Q R M F V M L	P C G G V G E L A T	L S A F I L A S L A P	T V P Q G L I S R V S	W G L K P P P G P N	P K S R P A P C P W	G P G R G V G T T P	1000
1001	L G P G S C V K P W	M M R A L T L A P Q	V D T D T I W N E L	H S S N A A R W A A	G S V T D L A F K V	A S R E L K N G F A	V V R P P G H H A D	H S T A M G F C F F	N S V A I A C R Q L	Q Q Q S K A S K I L	1100
1101	I V D W D V H H G N	G T Q Q T F Y Q D P	S V L Y I S L H R H	D D G N E F P G S G	A V D E V G A G S G	E G F N V N V A W A	G G L D P P M G D P	E Y L A A F R I V V	M P I A R E F S P D	L V L V S A G F D A	1200
1201	A E G H P A P U G G	Y H V S A K C F G Y	M T Q Q L M N L A G	G A V V I A L E G G	H D L T A I C D A S	E A C V A A L L G N	R V D P L S E E G W	K Q K P N L N A I R	S I L E A V I R V H S	K C G D G T L A E L	1300
1301	R L K D L G G T L P	H R G Q I L G F R C	Q P G D L L L W S	K I P V S D P G S N	G E H P P V R G Y P	L S P P D G A S R A	Y Q T V A P Q G K Y	W G C M Q R L A S C	P D S M V P R V P G	A D K E E V E A V T	1400
1401	A L A S I L S V G I L	.A E D R P S E Q L V	E E E E P M N L								
	10	20	30	40	50	60	70	80	90	100	
											1428

Fig. 6

cloned	1	- - - - -
deduced		M F A R S A G L C F P W Y P G Y S H G G D A E E Y L A Q H P T P T
cloned	1	- - - - -
deduced	34	G R G A E R R P R P P D S S A E G D P G M L K P C G C Y P S P Q K
cloned	1	- - - - -
deduced	67	Y A L K V G A P F C T C G C F Q R F H L P K A C P G Q Q G S P E S
cloned	1	- - - - -
deduced	100	A R P R N R Q P Y A T O N G P A P R P Q Y L P G S S S R C C H G Y
cloned	1	- - - - -
deduced	133	I C F L F D S S O T A E Y E Y G W G G D T G S Q L R P L L R G A Y
cloned	1	- - - - -
deduced	166	Y N S R M W D S Q K E D S K P D I L R L Q N T Q L F H S Y S L S T
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deduced	199	D G T O Y S P G A H Y C S P T G A G C P R P C A D T P G P Q P Q P
cloned	1	- - - - -
deduced	232	M D L R Y G Q R P P Y E P P P E P T L L A L Q R P Q R L H H H L F
cloned	1	- - - - -
deduced	265	L A G L Q Q Q R S Y E P M R Y K M E L P A C G A T L S L Y P S L P
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deduced	298	A F S I P R H Q S Q S S T P C P F L G C R P C P Q L S M D T P M P

Fig. 7

cloned	1	- - - - -
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cloned	1	- - - - -
deduced	400	L K Q P W H S F C R T L E P L E T E G A T R S M L S S F L P P V P
cloned	1	- - - - -
deduced	463	S L P S D P P E H F P L R K T Y S E P N L K L R Y K P K K S L E R
cloned	1	- - - - -
deduced	496	R K N P L L R K E S A P P S L R R R P A E T L G D S S P S S S T
cloned	1	- - - - -
deduced	529	P A S G C S S P N D S E H G P N P I L G S E A L L G Q R L R L Q E
cloned	1	- - - - -
deduced	562	T S Y A P F A L P T Y S L L P A I T L G L P A P A R A D S D R R T
cloned	1	- - - - -
deduced	595	H P T L G P R G P I L G S P H T P L F L P H G L E P E A G G T L P
cloned	1	- - - - -
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Fig. 7 (a)

11/19

cloned	1	-----
deduced	661	SLMTTERLSGSGLHWPLSRTSEPLPPSATAPP
cloned	1	-----
deduced	694	PPGPMQPRLEOLKTHYVOYIKRSAKPSEKPRLRO
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deduced	727	IPSAEDELETDOGGPGQVYDDGLEEHRELGHGOPE
cloned	58	ARGPAPLOOHPQYLLWEQQRLAGRLPRGSTGDT
deduced	760	ARGPAPLOOHPQYLLWEQQRLAGRLPRGSTGDT
cloned	91	YLLPLAOGGHRPLSRAOSSPAAPASLSAPEPAS
deduced	793	YLLPLAOGGHRPLSRAOSSPAAPASLSAPEPAS
cloned	124	QARYLSSSETPARTLPFTTGLIYDSYMLKHOCS
deduced	826	QARYLSSSETPARTLPFTTGLIYDSYMLKHOCS
cloned	157	CGDNSRHPEHAGRIQS IWSRLOERGLRSQCECL
deduced	859	CGDNSRHPEHAGRIQS IWSRLOERGLRSQCECL
cloned	190	RGRKASLEELQSYHSERHYLLYGTNPLSRLKLD
deduced	892	RGRKASLEELQSYHSERHYLLYGTNPLSRLKLD

Fig. 7 (b)

cloned	223	NGKLAGLLAQRMFYMLPCGGYG	- - - - -
deduced	923	NGKLAGLLAQRMFYMLPCGGYG	PLATLSAFLAS
cloned	245	- - - - -	- - - - -
deduced	958	LAPTYPQGLSRYSWGLKPPPGPNPKSRPAPCPW	
cloned	245	- - - - -	VDT
deduced	991	GPGRGYGTTPPLGPSCVKPWMMRALTLAPQYDT	
cloned	248	DTIWNELHSSNAARWAAGSYTDLAFKYASRELK	
deduced	1024	DTIWNELHSSNAARWAAGSYTDLAFKYASRELK	
cloned	281	NGFAYYRPPGHHADHSTAMGFCFFNSYAIACRQ	
deduced	1057	NGFAYYRPPGHHADHSTAMGFCFFNSYAIACRQ	
cloned	314	LQQOSKASKILIVDWDYHHGNGTQQTFYQDPSY	
deduced	1090	LQQOSKASKILIVDWDYHHGNGTQQTFYQDPSY	
cloned	347	LYISLHRHDDGNFFPGSGAYDEYGAGSGEGFNY	
deduced	1123	LYISLHRHDDGNFFPGSGAYDEYGAGSGEGFNY	
cloned	380	NYAWAGGLDPPMGDPEYLAAFRIVYMPIAREFS	
deduced	1156	NYAWAGGLDPPMGDPEYLAAFRIVYMPIAREFS	

Fig. 7 (c)

cloned	413	PDL YLYSAGFDAAEQHPAPLGGYHYSAKCFGYM
deduced	1189	PDL YLYSAGFDAAEQHPAPLGGYHYSAKCFGYM
cloned	446	TQQLMNLAGGAYYLAL EGGHDLTAICDASEACY
deduced	1222	TQQLMNLAGGAYYLAL EGGHDLTAICDASEACY
cloned	479	AALLGNRYDPLSEEQWKOKPNLNSIRSLEAVIR
deduced	1255	AALLGNRYDPLSEEQWKOKPNLNPAIRSLEAVIR
cloned	512	YHS-----
deduced	1288	YHS KCGDGTLAELRLKDLGGTLPHRGQILGFRC
cloned	515	-----
deduced	1321	QPGDLLLYWSKIPYSDPGSNGEHPPYRGYPLSP
cloned	515	-----
deduced	1354	PDGASRAYQTYAPQG KYWGMQRLASCPDSWYP
cloned	533	RYPGADKEEYEAYTALASLSYGILAEDRPSEQL
deduced	1387	RYPGADKEEYEAYTALASLSYGILAEDRPSEQL
cloned	566	YEEEEPML
deduced	1420	YEEEEPML

Fig. 7 (d)

14/19

227 PQQPQPMMDLRVGQR... PPVEP.... PPEPTLLALQRQQLHHHLFLAGL 268  
| : ||||| : :: | : || : ||| : |||:: | : ::::: | :  
44 PSAVPMDLRLDHQFSLPVAEPALREQQLQQELLALKQKQQIQRQILIAEF 93

269 QQQRSV..... EPMRVKMELPACGATLSLVPSLPAFSIPRHQSQS 308  
| :| : | : | : | : | : | : | : | : | : | : | : | : | : | :  
94 QRQHEQLSRQHEAQLHEHIKQQQEMLAMKHQQELLEH.. QRKLERHRQEQ 141

309 STPCPFLGCRPCPQLSMDTMPPELQVGPQEQLRQLLHKDKSKRSKEVAT 358  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
142 ..... ELEKQHREQKLQQLKNKEKGKES.... 164

359 PAQPSPTSQVPAAACVACAVASSVVKQKLAEVILKKQQAALERTVHPNSP 408  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
165 ..... AVASTEVKMKLQEfvLNKKKALAHRLN.... 191

409 GIPYRSQGPCSGQCPCSVPTPLKQPWHSFCRTLEPLETEGATR.SMLSSF 457  
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
192 ..... NHCISSDPRYWYGKTQHSSLQDS 214

458 LPPVPSLPS..... DPPEHFPLRKTVSEPNLKLRYKPK.KSLERR 496  
| | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
215 SPPQSGVSTSYNHPVLGMYDAKDDFPLRKTAEPNLKLRSRLKQKVAERR 264

497 KNPLLRRKESAP.. PSLRRRPAETLGDSSPSSSTPASGCSSPNDS.... 539  
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
265 SSPLLRRKDGPVVTAALKRPLDV... TDSACSSAPGSGPSSPNNSSGSVS 311

540 .EHGPNPILGS.. EALLGQRLRLQETSVAFFALPTVSLPAITLGLPA. 584  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
312 AENGIAPAVPSIPAETSLAHRLVAREGSAAPLPLYTSPSLPNITLGLPAT 361

585 ..... PARADSDRRTHPTLGPRGPILGSPH.TPLFLPHGLEPEAGGTLP 627  
: | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
362 GPSAGTAGQQDTERLTLPALQQRSLFPGTHLTPYLSTSPLERDGGAHS 411

628 SRLQPILLDPSGSHAPLLTVPGLGPLPFHFAQSLMTTERLSGS.... GL 673  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
412 PLLQHMVILLEQPPAQAPLVT.. GLGALPLH.AQSLVGADRVSPSIHKLRQ 458

674 HWPLSRTTRSEPLPPSATAPPNGPMQPRLEQLKTH.... VQVIKRS 715  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
459 HRPLGRTQSAPLPQNAQALQHLVIQQQHQQFLEKHKQQFQQQQLQMNKII 508

716 AKPSE..... KPRLRQIPSADLETGGGPG 741  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
509 PKPSEPARQPESHPEETEEELREHQALLDEPYLDRLPGQKEAHQAQAG.. V 556

742 QVVDDGLEHRELGHQPEARGP... APLQQHP..... QVILLWEQQR 779  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
557 QVKQEPIESDE.... EEAEPREVEPGQRQPSEQELLFRQQALLLEQQR 601

780 LAGRLPRGSTGDTVLLPLAQGGHRPLSRAQSSPA.APASLSAPEPASQAR 828  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
602 IHQLRNYQASMEAAGIPVSFGGHRPLSRAQSSPASATFPVSVQEPPTKPR 651

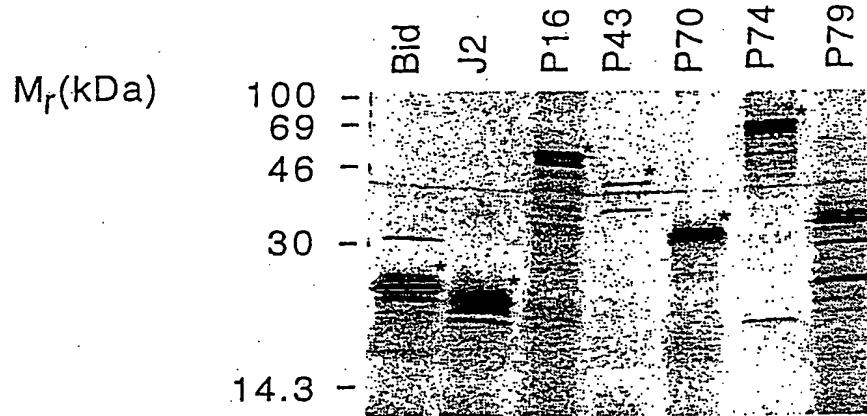
829 VLSSSETPARTLPFTTGLIYDSVMLKHQCSCGDNCSRHPFHAGRIQSIWSR 878  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
652 FTTGLVYDTMLKHZCTCGSSSSHPEHAGRIQSIWSR 688

879 LQERGLRSQCECLRGRKASLEELQSVHSERHVLLYGTNPLSRLKLDNGKL 928  
 ||| ||||:||||:||||:||||:||||:||||:||||:|||:  
 689 LQETGLRGKCECIRGRKATLEELQTVHSEAHTLLYGTNPLNRQKLDISKL 738  
 | ||: :||| |||||  
 929 AGLLAQRMFVMLPCGGVGPLATLSAFLASLAPTVPOGLSRVSWGLKPPPG 978  
 | ||: :||| |||||  
 739 LGSLAS.VFVRLPCGGVG..... 755  
 | ||: :||| |||||  
 979 PNPKSRPAPCPWGPGRGVGTTPLGPGSCVKPWMMRALTLPQVDTDTIWN 1028  
 | ||: :||| |||||  
 756 ..... VDSDTIWN 763  
 | ||: :||| |||||  
 1029 ELHSSNAARWAAGSVTDLAFKVASRELKNGFAVVRPPGHADHSTAMGFC 1078  
 | :|||:||| |||: |||: |||: |||: |||: |||: |||: |||: |||:  
 764 EVHSAGAARLAVGCVVELVFVKVATGELKNGFAVVRPPGHAEESTPMGFC 813  
 | :|||:||| |||: :|||: |||: |||: |||: |||: |||: |||:  
 1079 FFNSVAIACRQLQQQSKASKILIVDWDVHHNGTQQTFYQDPSVLYISLH 1128  
 :|||:|||:|||: :|||: |||: |||: |||: |||: |||: |||:  
 814 YFNSVAVAALKLQQRLSVSKILIVDWDVHHNGTQQAFYSDPSVLYMSLH 863  
 | :|||:|||:|||:|||:  
 1129 RHDDGNFFPGSGAVDEVGAGSGEGFNVNVAWAGGLDPPMGDPEYLAAFRI 1178  
 | :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 864 RYDDGNFFPGSGAPDEVGTGPVGFGNVNMAFTGGLDPPMGDAEYLAAFRT 913  
 | :|||:|||:|||:  
 1179 VVMPPIAREFSPDLVLVSAGFDAAEGHPAPLGGYHVSACKCFGYMTQQLMNL 1228  
 | :|||:|||:|||:|||:|||:|||:|||:|||:|||:  
 914 VVMPPIASEFAPDVVLVSSGFDAVEGHPTLGGYNLSARCFGYLTQQLMGL 963  
 | :|||:|||:  
 1229 AGGAVVIALEGGHDLTAICDASEACVAALLGNRVDPLSEEGWKQKPNLNA 1278  
 | :|||:|||:|||:|||:|||:|||:|||:|||:  
 964 AGGRIVVIALEGGHDLTAICDASEACVSALLGNELDPLPEKVLQQRPNANA 1013  
 | :|||:|||:  
 1279 IRSLEAVIRVHSKCGDGTIAELRLKDLGGTLPHRGQILGFRCQPGDLLL 1328  
 :|||:|||:  
 1014 VRSMEKVMEIHS..... 1025  
 | :|||:  
 1329 WSKIPVSDPGSNGEHPPVRYPLSPPDGASRAYQTVAPOQKYWGCMQRLA 1378  
 | :|||:  
 1026 ..... KYWRCLQRTT 1035  
 | :|||:  
 1379 SCPDSWVPRVPGADKEEVEAVTALASLSVGIL.AEDRPSEQLVEEEPM 1426  
 | :|||:  
 1036 STAGRSLIEAQTCENEAEVTAMASLSVGVKPAEKRPDEEPMEEPPL 1084

Fig. 8 (a)

16/19

A



B

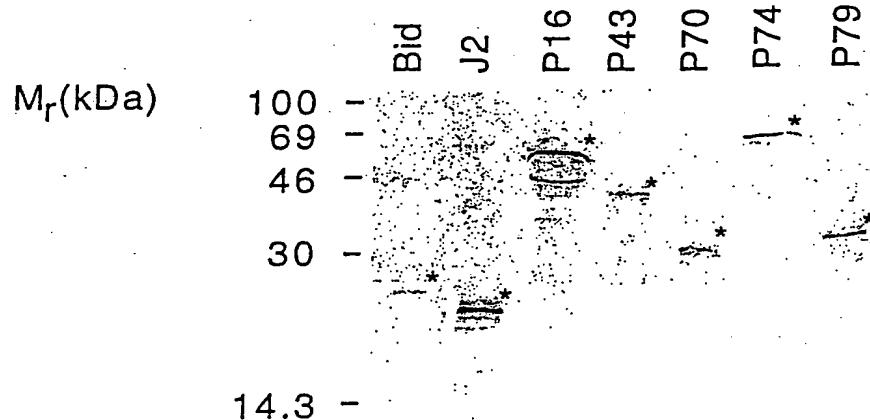


Fig. 9

17/19

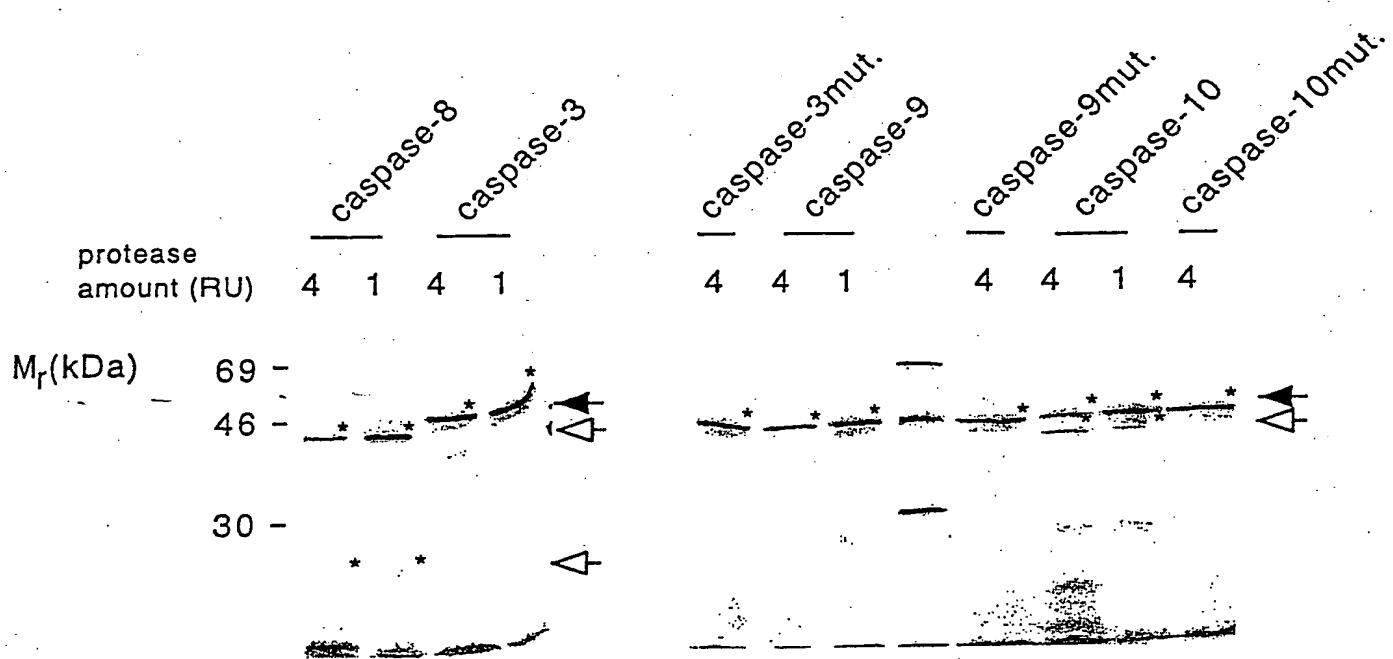


Fig. 10

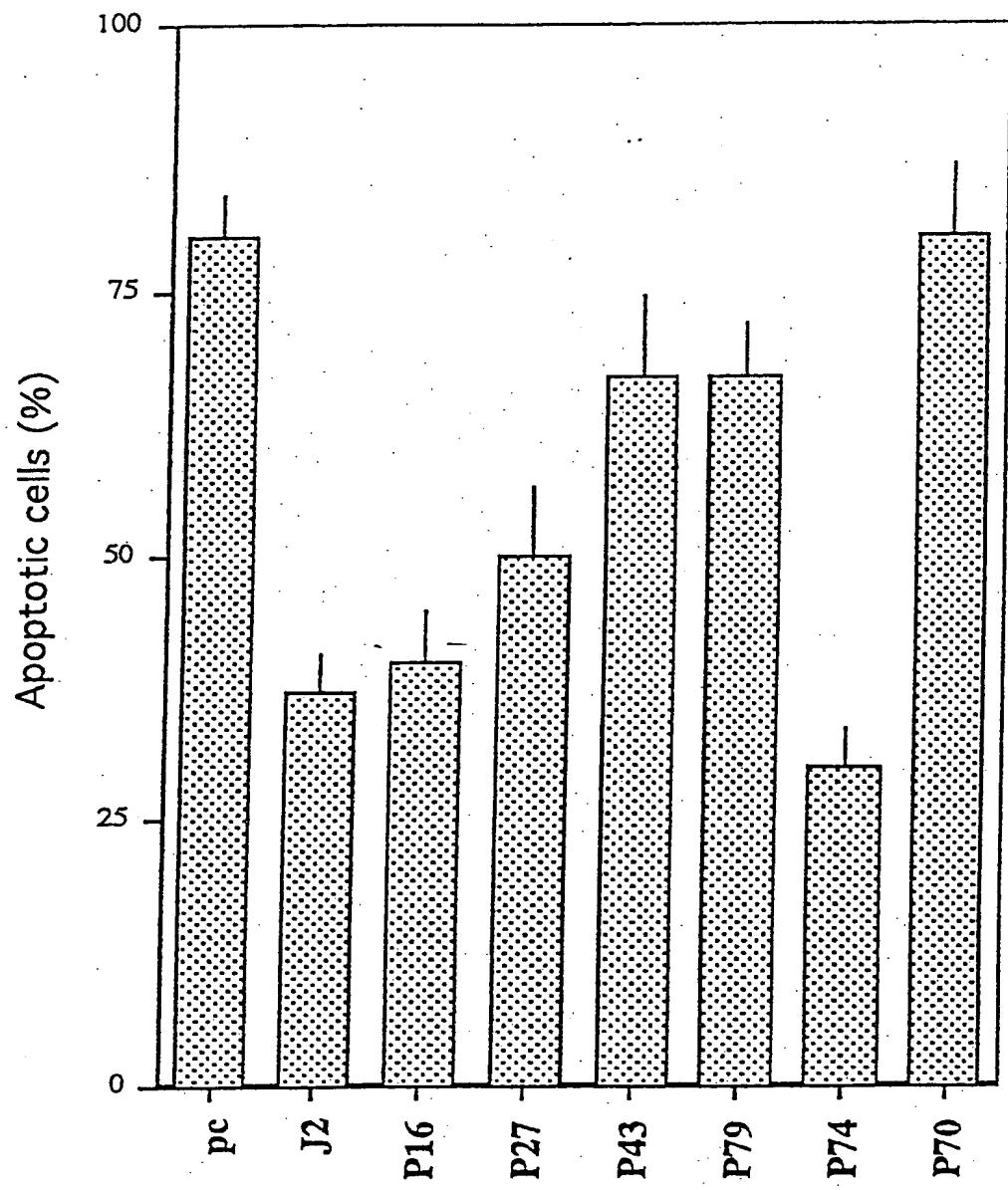


Fig. 11

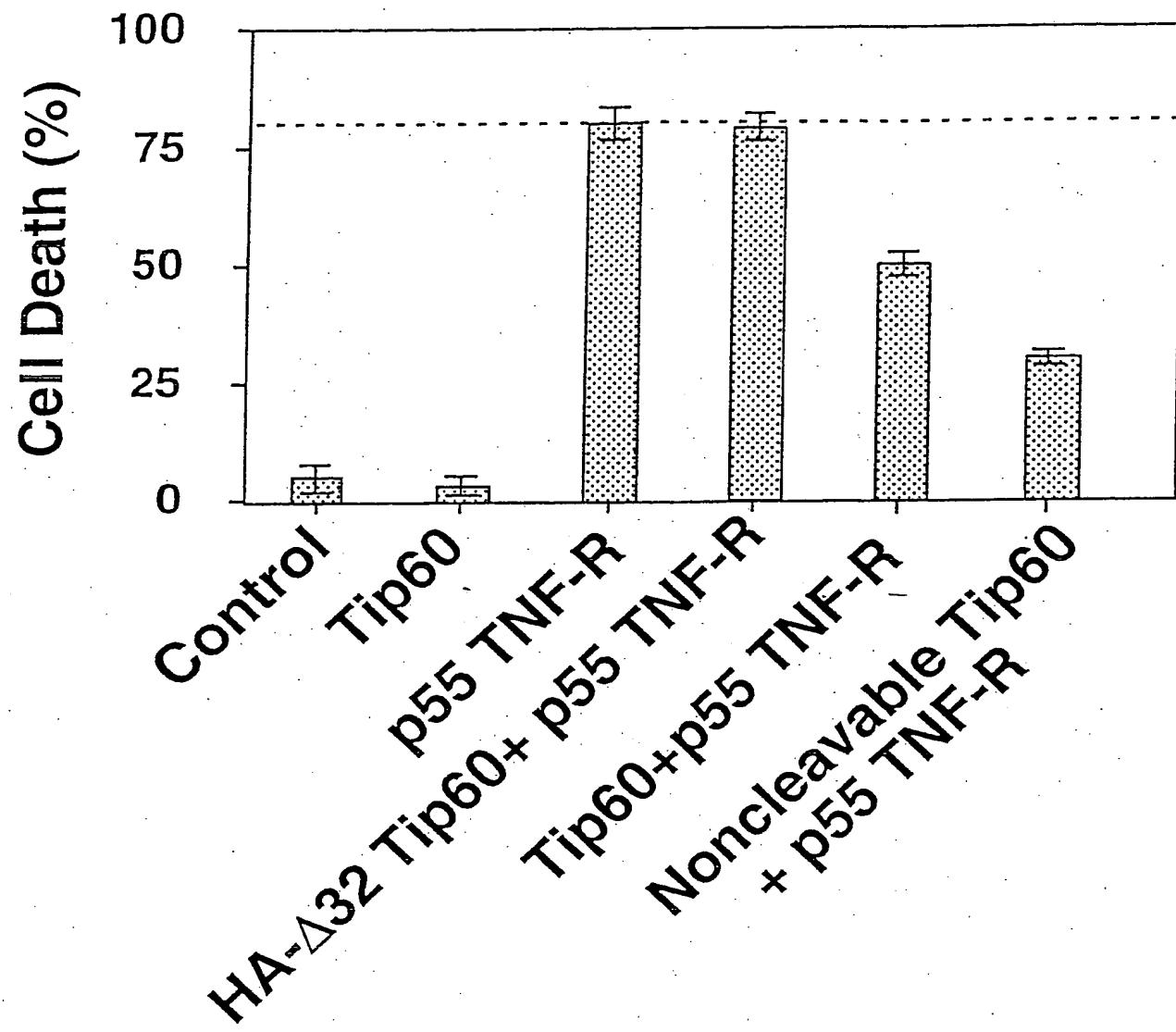


Fig. 12